

Tue Jul 17 14:07:15 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]
Repeats masked. (summary below)
/home/ruby/va/Molbio/carpenda/temp1/ss.DNA37151 (3679 bp)

(A)

TECH CENTER

APR 05 2002

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1-A SHINSHI 1547

Sequences producing High-scoring Segment Pairs:

		Frame	Score	Match	Pct	E
1	P_AAF72414 Human PRO293 cDNA.	+	3679	3679	100	0.0
2	P_AAX52256 Protein PRO293 cDNA clone DNA37151-1193.	+	3679	3679	100	0.0
3	AC021462 Homo sapiens clone RP11-276C1, WORKING D	+	3658	3670	100	0.0
4	AL512306 Homo sapiens chromosome 1 clone RP11-430	-	3658	3670	100	0.0
5	NM_006338 Homo sapiens glioma amplified on chromos	+	3002	3017	100	0.0
6	AF030435 Homo sapiens glioma amplified on chromos	+	3002	3017	100	0.0

>1 P_AAF72414 Human PRO293 cDNA. (3679 bp) [1 seg]

Score = 3679 (7293 bits), Expect = 0.0

Identities = 3679/3679 (100%), at 1,1-3679,3679, Strand +/-

```
DNA37151      1  AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG
*****
P_AAF72414    1  AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG

DNA37151     61  CTCAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAA
*****
P_AAF72414    61  CTCAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAA

DNA37151    121  CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAA
*****
P_AAF72414   121  CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAA

DNA37151    181  GACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGAC
*****
P_AAF72414   181  GACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGAC

DNA37151    241  AGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG
*****
P_AAF72414   241  AGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG

DNA37151    301  CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATC
*****
P_AAF72414   301  CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATC

DNA37151    361  ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTA
*****
P_AAF72414   361  ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTA

DNA37151    421  AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG
*****
P_AAF72414   421  AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG

DNA37151    481  CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG
*****
P_AAF72414   481  CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG

DNA37151    541  CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
*****
P_AAF72414   541  CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA

DNA37151    601  GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACCTCTGCATCCTCTTCTTCCAGGGCTGC
*****
P_AAF72414   601  GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACCTCTGCATCCTCTTCTTCCAGGGCTGC

DNA37151    661  CCCTGATGGGGCCTGGCAATGACTGAGCAGGCCCAGCCCCAGAGGACAAGGAAGAGAAGG
*****
P_AAF72414   661  CCCTGATGGGGCCTGGCAATGACTGAGCAGGCCCAGCCCCAGAGGACAAGGAAGAGAAGG
```

DNA37151	721	CATATTGAGGAGGGCAAGAAGTGACGCCCCGGTGTAGAAATGACTGCCCTGGGAGGGTGGTT
P_AAF72414	721	CATATTGAGGAGGGCAAGAAGTGACGCCCCGGTGTAGAAATGACTGCCCTGGGAGGGTGGTT
DNA37151	781	CCTTGGGCCCTGGCAGGGTTGCTGACCCCTTACCCTGCAAAACACAAAGAGCAGGACTCCA
P_AAF72414	781	CCTTGGGCCCTGGCAGGGTTGCTGACCCCTTACCCTGCAAAACACAAAGAGCAGGACTCCA
DNA37151	841	GACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
P_AAF72414	841	GACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
DNA37151	901	ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCCGTGGTACCCTGGCATGT
P_AAF72414	901	ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCCGTGGTACCCTGGCATGT
DNA37151	961	TCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTTA
P_AAF72414	961	TCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTTA
DNA37151	1021	CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTTGACGGCAGTCCCCCGGCACT
P_AAF72414	1021	CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTTGACGGCAGTCCCCCGGCACT
DNA37151	1081	CCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTGGACCAGAG
P_AAF72414	1081	CCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTGGACCAGAG
DNA37151	1141	TGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA
P_AAF72414	1141	TGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA
DNA37151	1201	TGCCCCGAGACTGTGATTTCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAA
P_AAF72414	1201	TGCCCCGAGACTGTGATTTCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAA
DNA37151	1261	CCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTTA
P_AAF72414	1261	CCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTTA
DNA37151	1321	TCTCAACCACAACCAGCTCTACCGCATCGCCCCCAGGGCCTTTTCTGGCCTCAGCAACTT
P_AAF72414	1321	TCTCAACCACAACCAGCTCTACCGCATCGCCCCCAGGGCCTTTTCTGGCCTCAGCAACTT
DNA37151	1381	GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGGTTTGAAT
P_AAF72414	1381	GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGGTTTGAAT
DNA37151	1441	GCTGCCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
P_AAF72414	1441	GCTGCCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
DNA37151	1501	GAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGA
P_AAF72414	1501	GAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGA
DNA37151	1561	GATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAA
P_AAF72414	1561	GATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAA
DNA37151	1621	CCAGCTGGCCCCGGGTGCCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTTCCTAGA
P_AAF72414	1621	CCAGCTGGCCCCGGGTGCCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTTCCTAGA

BLAST RESULTS A-2

DNA37151 1681 CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGCACCT

P_AAF72414 1681 CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGCACCT

DNA37151 1741 TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT

P_AAF72414 1741 TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT

DNA37151 1801 GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA

P_AAF72414 1801 GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA

DNA37151 1861 CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCT

P_AAF72414 1861 CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCT

DNA37151 1921 CAGTGCCTTGACACCAGCAGACGGTGGAGTCCCTGCCCAACCTGCAGGAGGTAGGTCTCCA

P_AAF72414 1921 CAGTGCCTTGACACCAGCAGACGGTGGAGTCCCTGCCCAACCTGCAGGAGGTAGGTCTCCA

DNA37151 1981 CGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGT

P_AAF72414 1981 CGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGT

DNA37151 2041 CCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC

P_AAF72414 2041 CCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC

DNA37151 2101 GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCCTCATCTCCCCACG

P_AAF72414 2101 GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCCTCATCTCCCCACG

DNA37151 2161 AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC

P_AAF72414 2161 AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC

DNA37151 2221 ACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC

P_AAF72414 2221 ACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC

DNA37151 2281 TGCCCATGCAGGCAGGAGGTACCGGGTGTAACCCGAGGGGACCCGAGCTGCGGAGGGT

P_AAF72414 2281 TGCCCATGCAGGCAGGAGGTACCGGGTGTAACCCGAGGGGACCCGAGCTGCGGAGGGT

DNA37151 2341 GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGGGCTGACAC

P_AAF72414 2341 GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGGGCTGACAC

DNA37151 2401 TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACA

P_AAF72414 2401 TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACA

DNA37151 2461 GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTACAC

P_AAF72414 2461 GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTACAC

DNA37151 2521 CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCCTCCTCCCTCCGGGGCCA

P_AAF72414 2521 CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCCTCCTCCCTCCGGGGCCA

DNA37151 2581 GGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTACAACATTACCCGCCT

P_AAF72414 2581 GGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTACAACATTACCCGCCT

DNA37151	2641	CCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCCACACCCA
P_AAF72414	2641	CCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCCACACCCA
DNA37151	2701	GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGA
P_AAF72414	2701	GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGA
DNA37151	2761	TCGTCCTGGGCTCATTGCCATCCTGGCTCTCGCTGTCCTTCTCCTGGCAGCTGGGCTAGC
P_AAF72414	2761	TCGTCCTGGGCTCATTGCCATCCTGGCTCTCGCTGTCCTTCTCCTGGCAGCTGGGCTAGC
DNA37151	2821	GGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCTCTCCCTCC
P_AAF72414	2821	GGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCTCTCCCTCC
DNA37151	2881	AGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGTTGTGTCTGCTCCCCCTCGT
P_AAF72414	2881	AGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGTTGTGTCTGCTCCCCCTCGT
DNA37151	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC
P_AAF72414	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC
DNA37151	3001	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
P_AAF72414	3001	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
DNA37151	3061	CTACTTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
P_AAF72414	3061	CTACTTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
DNA37151	3121	ACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGGCCCTGGGG
P_AAF72414	3121	ACCCACGTGCTTGAGGCCTGGGAGCTGGGCCAAGACAGATGGGGCTTTGTGGCCCTGGGG
DNA37151	3181	GTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATTC
P_AAF72414	3181	GTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATTC
DNA37151	3241	TGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT
P_AAF72414	3241	TGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT
DNA37151	3301	CTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGCTGTCCCCTACCTGTGTCCCCGGGCTG
P_AAF72414	3301	CTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGCTGTCCCCTACCTGTGTCCCCGGGCTG
DNA37151	3361	CACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGCCTCCTGGG
P_AAF72414	3361	CACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGCCTCCTGGG
DNA37151	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGTGGGAGTGA
P_AAF72414	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGTGGGAGTGA
DNA37151	3481	CCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCCAGGAACGCCTCATCTCAGCA
P_AAF72414	3481	CCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCCAGGAACGCCTCATCTCAGCA
DNA37151	3541	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCATAGGCAATTTTGTACCTTTGTGGAGAA
P_AAF72414	3541	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCATAGGCAATTTTGTACCTTTGTGGAGAA

BLAST RESULTS A-A

BLAST RESULTS A-5

```
DNA37151 3601 ATGTGTCACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATA
*****
P_AAF72414 3601 ATGTGTCACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATA

DNA37151 3661 AATAATAACAATAAAAAAA
*****
P_AAF72414 3661 AATAATAACAATAAAAAAA

>2 P_AAX52256 Protein PRO293 cDNA clone DNA37151-1193. DNA, PAT 25-JUN-1999
(3679 bp) [1 seg]
Score = 3679 (7293 bits), Expect = 0.0
Identities = 3679/3679 (100%), at 1,1-3679,3679, Strand +/-

DNA37151 1 AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG
*****
P_AAX52256 1 AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG

DNA37151 61 CTCAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAA
*****
P_AAX52256 61 CTCAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAA

DNA37151 121 CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAA
*****
P_AAX52256 121 CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAA

DNA37151 181 GACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGAC
*****
P_AAX52256 181 GACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGAC

DNA37151 241 AGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG
*****
P_AAX52256 241 AGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG

DNA37151 301 CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATC
*****
P_AAX52256 301 CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATC

DNA37151 361 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTA
*****
P_AAX52256 361 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTA

DNA37151 421 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCGTGTAATCCCAGCTACTCAGGTGG
*****
P_AAX52256 421 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCGTGTAATCCCAGCTACTCAGGTGG

DNA37151 481 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG
*****
P_AAX52256 481 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG

DNA37151 541 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
*****
P_AAX52256 541 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA

DNA37151 601 GGGGTAGATACTGCTTCTCTGCAACCTCCTTAAGTCTGCATCCTCTTCTTCCAGGGCTGC
*****
P_AAX52256 601 GGGGTAGATACTGCTTCTCTGCAACCTCCTTAAGTCTGCATCCTCTTCTTCCAGGGCTGC

DNA37151 661 CCCTGATGGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGG
*****
P_AAX52256 661 CCCTGATGGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGG

DNA37151 721 CATATTGAGGAGGGCAAGAAGTGACGCCCCGGTGTAGAATGACTGCCCTGGGAGGGTGGTT
*****
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P_AAX52256	721	CATATTGAGGAGGGCAAGAAGTGACGCCCGGTGTAGAATGACTGCCCTGGGAGGGTGGTT
DNA37151	781	CCTTGGGCCCTGGCAGGGTTGCTGACCCCTACCCTGCAAAACACAAAGAGCAGGACTCCA *****
P_AAX52256	781	CCTTGGGCCCTGGCAGGGTTGCTGACCCCTACCCTGCAAAACACAAAGAGCAGGACTCCA
DNA37151	841	GACTCTCCTTGTGAATGGTCCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC *****
P_AAX52256	841	GACTCTCCTTGTGAATGGTCCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
DNA37151	901	ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCCTGGCATGT *****
P_AAX52256	901	ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCCTGGCATGT
DNA37151	961	TCCCTGCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCCTA *****
P_AAX52256	961	TCCCTGCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCCTA
DNA37151	1021	CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTGACGGCAGTCCCCCGGCACT *****
P_AAX52256	1021	CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTGACGGCAGTCCCCCGGCACT
DNA37151	1081	CCCCGAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTGGACCAGAG *****
P_AAX52256	1081	CCCCGAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTGGACCAGAG
DNA37151	1141	TGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA *****
P_AAX52256	1141	TGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA
DNA37151	1201	TGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAA *****
P_AAX52256	1201	TGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAA
DNA37151	1261	CCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTCTA *****
P_AAX52256	1261	CCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTCTA
DNA37151	1321	TCTCAACCACAACCAGCTCTACCGCATCGCCCCCAGGGCCTTTTCTGGCCTCAGCAACTT *****
P_AAX52256	1321	TCTCAACCACAACCAGCTCTACCGCATCGCCCCCAGGGCCTTTTCTGGCCTCAGCAACTT
DNA37151	1381	GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGGTTTGAAT *****
P_AAX52256	1381	GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGGTTTGAAT
DNA37151	1441	GCTGCCCCAATTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT *****
P_AAX52256	1441	GCTGCCCCAATTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
DNA37151	1501	GAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGA *****
P_AAX52256	1501	GAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGA
DNA37151	1561	GATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAA *****
P_AAX52256	1561	GATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAA
DNA37151	1621	CCAGCTGGCCCCGGGTGCCAGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTTCTTAGA *****
P_AAX52256	1621	CCAGCTGGCCCCGGGTGCCAGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTTCTTAGA
DNA37151	1681	CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTTGCCAACATGCTGCACCT *****

BLAST RESULTS A-U

P_AAX52256 1681 CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGCACCT
DNA37151 1741 TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT

P_AAX52256 1741 TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT
DNA37151 1801 GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCTTCATCCA

P_AAX52256 1801 GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCTTCATCCA
DNA37151 1861 CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCTCATGCTCAACAACAACGCTCT

P_AAX52256 1861 CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCTCATGCTCAACAACAACGCTCT
DNA37151 1921 CAGTGCCTTGACACCAGCAGACGGTGGAGTCCCTGCCCAACCTGCAGGAGGTAGGTCTCCA

P_AAX52256 1921 CAGTGCCTTGACACCAGCAGACGGTGGAGTCCCTGCCCAACCTGCAGGAGGTAGGTCTCCA
DNA37151 1981 CGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGT

P_AAX52256 1981 CGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGT
DNA37151 2041 CCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC

P_AAX52256 2041 CCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC
DNA37151 2101 GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCTCATCTCCCCACG

P_AAX52256 2101 GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCTCATCTCCCCACG
DNA37151 2161 AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC

P_AAX52256 2161 AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC
DNA37151 2221 ACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC

P_AAX52256 2221 ACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC
DNA37151 2281 TGCCCATGCAGGCAGGAGGTACCGGGTGTAACCCGAGGGGACCTTGAGCTGCGGAGGGT

P_AAX52256 2281 TGCCCATGCAGGCAGGAGGTACCGGGTGTAACCCGAGGGGACCTTGAGCTGCGGAGGGT
DNA37151 2341 GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACC'TGGTGGGGGCTGACAC

P_AAX52256 2341 GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACC'TGGTGGGGGCTGACAC
DNA37151 2401 TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACA

P_AAX52256 2401 TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACA
DNA37151 2461 GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTAC

P_AAX52256 2461 GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTAC
DNA37151 2521 CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTCCGGGGCCA

P_AAX52256 2521 CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTCCGGGGCCA
DNA37151 2581 GGGGGCCACAGCTCTGGCCCGCTGCCTCGGGGAACCCACAGCTACAACATTACCCGCCT

P_AAX52256 2581 GGGGGCCACAGCTCTGGCCCGCTGCCTCGGGGAACCCACAGCTACAACATTACCCGCCT
DNA37151 2641 CCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCACACCCA

BLAST RESULTS A-7

P_AAX52256	2641	CCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCCACACCCA
DNA37151	2701	GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGA
P_AAX52256	2701	GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGA
DNA37151	2761	TCGTCCTGGGCTCATTGCCATCCTGGCTCTCGCTGTCTTCTCTCGGCTGGGCTAGC
P_AAX52256	2761	TCGTCCTGGGCTCATTGCCATCCTGGCTCTCGCTGTCTTCTCTCGGCTGGGCTAGC
DNA37151	2821	GGCCACCTTGCCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCTCTCCCTCC
P_AAX52256	2821	GGCCACCTTGCCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCTCTCCCTCC
DNA37151	2881	AGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGTGTCTGCTCCCTCGT
P_AAX52256	2881	AGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGTGTCTGCTCCCTCGT
DNA37151	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC
P_AAX52256	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC
DNA37151	3001	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
P_AAX52256	3001	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
DNA37151	3061	CTACTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
P_AAX52256	3061	CTACTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
DNA37151	3121	ACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGGCCCTGGGG
P_AAX52256	3121	ACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGGCCCTGGGG
DNA37151	3181	GTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATTC
P_AAX52256	3181	GTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATTC
DNA37151	3241	TGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCCTCCCCATCTT
P_AAX52256	3241	TGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCCTCCCCATCTT
DNA37151	3301	CTCTCTGCCCAGAGGCTCCTGGGCCGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTG
P_AAX52256	3301	CTCTCTGCCCAGAGGCTCCTGGGCCGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTG
DNA37151	3361	CACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGCCCTCTGGG
P_AAX52256	3361	CACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGCCCTCTGGG
DNA37151	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGTGGGAGTGA
P_AAX52256	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGTGGGAGTGA
DNA37151	3481	CCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCCTCATCTCAGCA
P_AAX52256	3481	CCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCCTCATCTCAGCA
DNA37151	3541	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
P_AAX52256	3541	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
DNA37151	3601	ATGTGTCACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATA

BLAST RESULTS A-2

P_AAX52256 3601 ATGTGTCACCTCCCCCAACCCGATTCACCTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATA
DNA37151 3661 AATAATAACAATAAAAAAA

P_AAX52256 3661 AATAATAACAATAAAAAAA

>3 AC021462 Homo sapiens clone RP11-276C1, WORKING DRAFT SEQUENCE, 21 unordered
(153023 bp) [1 seg]
Score = 3658 (7251 bits), Expect = 0.0
Identities = 3670/3674 (99%), at 1,129821-3674,133494, Strand +/-

DNA37151 1 AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG

AC021462 129821 AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG
DNA37151 61 CTCAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAA

AC021462 129881 CTCAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAA
DNA37151 121 CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAA

AC021462 129941 CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAA
DNA37151 181 GACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGAC

AC021462 130001 GACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGAC
DNA37151 241 AGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG

AC021462 130061 AGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG
DNA37151 301 CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATC

AC021462 130121 CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATC
DNA37151 361 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTA

AC021462 130181 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTA
DNA37151 421 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG

AC021462 130241 AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGG
DNA37151 481 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG

AC021462 130301 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG
DNA37151 541 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA

AC021462 130361 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
DNA37151 601 GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGC

AC021462 130421 GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGC
DNA37151 661 CCCTGATGGGGCCTGGCAATGACTGAGCAGGCCCGAGCCCAGAGGACAAGGAAGAGAAGG

AC021462 130481 CCCTGATGGGGCCTGGCAATGACTGAGCAGGCCCGAGCCCAGAGGACAAGGAAGAGAAGG
DNA37151 721 CATATTGAGGAGGGCAAGAAGTGACGCCCCGGTGTAAGAATGACTGCCCTGGGAGGGTGGTT

AC021462 130541 CATATTGAGGAGGGCAAGAAGTGACGCCCCGGTGTAAGAATGACTGCCCTGGGAGGGTGGTT
DNA37151 781 CCTTGGGCCCTGGCAGGGTTGCTGACCCCTACCCTGCAAAACACAAAGAGCAGGACTCCA

BLAST RESULTS A-9

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*****
AC021462 130601 CCTTGGGCCCTGGCAGGGTTGCTGACCCTTACCCTGCAAAACACAAAGAGCAGGACTCCA
DNA37151 841 GACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
*****
AC021462 130661 GACTCTTCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
DNA37151 901 ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCCGTGGTACCCTGGCATGT
*****
AC021462 130721 ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCCGCTGTGCCCGTGGTACCCTGGCATGT
DNA37151 961 TCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTTA
*****
AC021462 130781 TCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTTA
DNA37151 1021 CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTTGACGGCAGTCCCCCGGCACT
*****
AC021462 130841 CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTTGACGGCAGTCCCCCGGCACT
DNA37151 1081 CCCCAGGACACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTGGACCAGAG
*****
AC021462 130901 CCCCAGGACACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTGGACCAGAG
DNA37151 1141 TGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA
*****
AC021462 130961 TGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA
DNA37151 1201 TGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAA
*****
AC021462 131021 TGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAA
DNA37151 1261 CCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTTA
*****
AC021462 131081 CCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTTA
DNA37151 1321 TCTCAACCACAACCAGCTCTACGCGATCGCCCCCAGGGCCTTTTCTGGCCTCAGCAACTT
*****
AC021462 131141 TCTCAACCACAACCAGCTCTACGCGATCGCCCCCAGGGCCTTTTCTGGCCTCAGCAACTT
DNA37151 1381 GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGGTTTGAAAT
*****
AC021462 131201 GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGGTTTGAAAT
DNA37151 1441 GCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
*****
AC021462 131261 GCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
DNA37151 1501 GAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGA
*****
AC021462 131321 GAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGA
DNA37151 1561 GATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAA
*****
AC021462 131381 GATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAA
DNA37151 1621 CCAGCTGGCCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCCGGGCTCAAGTTCCTAGA
*****
AC021462 131441 CCAGCTGGCCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCCGGGCTCAAGTTCCTAGA
DNA37151 1681 CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGCACCT
*****
AC021462 131501 CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGCACCT
DNA37151 1741 TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT
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*****
AC021462 131561 TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT
DNA37151 1801 GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCTTCATCCA
*****
AC021462 131621 GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCTTCATCCA
DNA37151 1861 CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCT
*****
AC021462 131681 CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCT
DNA37151 1921 CAGTGCCTTGACACCAGCAGACGGTGGAGTCCCTGCCCAACCTGCAGGAGGTAGGTCTCCA
*****
AC021462 131741 CAGTGCCTTGACACCAGCAGACGGTGGAGTCCCTGCCCAACCTGCAGGAGGTAGGTCTCCA
DNA37151 1981 CGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGT
*****
AC021462 131801 CGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGT
DNA37151 2041 CCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC
*****
AC021462 131861 CCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC
DNA37151 2101 GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCTCATCTCCCCACG
*****
AC021462 131921 GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCTCATCTCCCCACG
DNA37151 2161 AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC
*****
AC021462 131981 AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC
DNA37151 2221 ACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC
*****
AC021462 132041 ACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC
DNA37151 2281 TGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCCTGGAGCTGCGGAGGGT
*****
AC021462 132101 TGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCCTGGAGCTGCGGAGGGT
DNA37151 2341 GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGGGCTGACAC
*****
AC021462 132161 GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGGGCTGACAC
DNA37151 2401 TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACA
*****
AC021462 132221 TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACA
DNA37151 2461 GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTGAC
*****
AC021462 132281 GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTGAC
DNA37151 2521 CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTCCGGGGCCA
*****
AC021462 132341 CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTCCGGGGCCA
DNA37151 2581 GGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTACAACATTACCCGCCT
*****
AC021462 132401 GGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTACAACATTACCCGCCT
DNA37151 2641 CCTTCAGGCCACGGAGTACTGGGCTGCCTGCAAGTGGCCTTTGCTGATGCCCACACCCA
*****
AC021462 132461 CCTTCAGGCCACGGAGTACTGGGCTGCCTGCAAGTGGCCTTTGCTGATGCCCACACCCA
DNA37151 2701 GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGA

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BLAST RESULTS A-11

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*****
AC021462 132521 GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGA
DNA37151 2761 TCGTCCTGGGCTCATTTGCCATCCTGGCTCTCGCTGTCTTCTCTGGCAGCTGGGCTAGC
*****
AC021462 132581 CCGTCCTGGGCTCATTTGCCATCCTGGCTCTCGCTGTCTTCTCTGGCAGCTGGGCTAGC
DNA37151 2821 GGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCTCTCCCTCC
*****
AC021462 132641 GGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCTCTCCCTCC
DNA37151 2881 AGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGTGTCTGCTCCCTCGT
*****
AC021462 132701 AGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGTGTCTGCTCCCTCGT
DNA37151 2941 CCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC
*****
AC021462 132761 CCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC
DNA37151 3001 ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
*****
AC021462 132821 ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
DNA37151 3061 CTACTTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
*****
AC021462 132881 CTACTTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
DNA37151 3121 ACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGGCCCTGGGG
*****
AC021462 132941 ACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGGCCCTGGGG
DNA37151 3181 GTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATTC
*****
AC021462 133001 GTGCTTCTGCAGCCTCGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATTC
DNA37151 3241 TGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCCTCCCCATCTT
*****
AC021462 133061 TGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCCTCCCCATCTT
DNA37151 3301 CTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTG
*****
AC021462 133121 CTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTG
DNA37151 3361 CACCCCTTCCTCTTCTCTTCTCTGTACAGTCTCAGTTGCTTGCCTCTTGTGCCCTCTGGG
*****
AC021462 133181 CACCCCTTCCTCTTCTCTTCTCTGTACAGTCTCAGTTGCTTGCCTCTTGTGCCCTCTGGG
DNA37151 3421 CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGTGGGAGTGA
*****
AC021462 133241 CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGTGGGAGTGA
DNA37151 3481 CCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCTCATCTCAGCA
*****
AC021462 133301 CCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCTCATCTCAGCA
DNA37151 3541 GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
*****
AC021462 133361 GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
DNA37151 3601 ATGTGTACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATA
*****
AC021462 133421 ATGTGTACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATA
DNA37151 3661 AATAATAACAATAA

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BLAST RESULTS A-12

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*****
AC021462 133481 AATAATAACAATAA

>4 AL512306 Homo sapiens chromosome 1 clone RP11-430C7, *** SEQUENCING IN
(185048 bp) [1 seg]
Score = 3658 (7251 bits), Expect = 0.0
Identities = 3670/3674 (99%), at 1,107156-3674,103483, Strand +/-

DNA37151      1 AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG
*****
AL512306 107156 AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG

DNA37151      61 CTCAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAA
*****
AL512306 107096 CTCAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAA

DNA37151     121 CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAA
*****
AL512306 107036 CACACATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAA

DNA37151     181 GACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGAC
*****
AL512306 106976 GACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGAC

DNA37151     241 AGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG
*****
AL512306 106916 AGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG

DNA37151     301 CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATC
*****
AL512306 106856 CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATC

DNA37151     361 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTA
*****
AL512306 106796 ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTA

DNA37151     421 AAAATACAAAATTAGCCAGGAGTGGTGGCAGGTGCCGTGAATCCCAGCTACTCAGGTGG
*****
AL512306 106736 AAAATACAAAATTAGCCAGGAGTGGTGGCAGGTGCCGTGAATCCCAGCTACTCAGGTGG

DNA37151     481 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG
*****
AL512306 106676 CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG

DNA37151     541 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
*****
AL512306 106616 CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA

DNA37151     601 GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGC
*****
AL512306 106556 GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGC

DNA37151     661 CCCTGATGGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGG
*****
AL512306 106496 CCCTGATGGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGG

DNA37151     721 CATATTGAGGAGGGCAAGAAGTGACGCCCGGTGTAGAATGACTGCCCTGGGAGGGTGGTT
*****
AL512306 106436 CATATTGAGGAGGGCAAGAAGTGACGCCCGGTGTAGAATGACTGCCCTGGGAGGGTGGTT

DNA37151     781 CCTTGGGCCCTGGCAGGGTTGCTGACCCTTACCCTGCAAAACACAAAGAGCAGGACTCCA
*****
AL512306 106376 CCTTGGGCCCTGGCAGGGTTGCTGACCCTTACCCTGCAAAACACAAAGAGCAGGACTCCA

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BLAST RESULTS A-13

DNA37151	841	GACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
AL512306	106316	GACTCTTCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
DNA37151	901	ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCCGTGGTACCCTGGCATGT
AL512306	106256	ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCCGCTGTGCCCCGTGGTACCCTGGCATGT
DNA37151	961	TCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCCTA
AL512306	106196	TCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCCTA
DNA37151	1021	CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTTGACGGCAGTCCCCCGGCACT
AL512306	106136	CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTTGACGGCAGTCCCCCGGCACT
DNA37151	1081	CCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTGGACCAGAG
AL512306	106076	CCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTGGACCAGAG
DNA37151	1141	TGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA
AL512306	106016	TGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA
DNA37151	1201	TGCCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAA
AL512306	105956	TGCCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAA
DNA37151	1261	CCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTCTA
AL512306	105896	CCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTCTA
DNA37151	1321	TCTCAACCACAACCAGCTCTACCGCATCGCCCCCAGGGCCTTTTCTGGCCTCAGCAACTT
AL512306	105836	TCTCAACCACAACCAGCTCTACCGCATCGCCCCCAGGGCCTTTTCTGGCCTCAGCAACTT
DNA37151	1381	GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGGTTTGAAT
AL512306	105776	GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGGTTTGAAT
DNA37151	1441	GCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
AL512306	105716	GCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
DNA37151	1501	GAACCTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGA
AL512306	105656	GAACCTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGA
DNA37151	1561	GATCTCCGACTATGCCCCGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAA
AL512306	105596	GATCTCCGACTATGCCCCGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAA
DNA37151	1621	CCAGCTGGCCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTTCCTAGA
AL512306	105536	CCAGCTGGCCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTTCCTAGA
DNA37151	1681	CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGCACCT
AL512306	105476	CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGCACCT
DNA37151	1741	TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT
AL512306	105416	TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT

BLAST RESULTS A-A

DNA37151	1801	GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA
AL512306	105356	GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA
DNA37151	1861	CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCT
AL512306	105296	CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCT
DNA37151	1921	CAGTGCCTTGCACCAGCAGACGGTGGAGTCCC TGCCCAACCTGCAGGAGGTAGGTCTCCA
AL512306	105236	CAGTGCCTTGCACCAGCAGACGGTGGAGTCCC TGCCCAACCTGCAGGAGGTAGGTCTCCA
DNA37151	1981	CGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGT
AL512306	105176	CGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGCACCCGTGT
DNA37151	2041	CCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC
AL512306	105116	CCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC
DNA37151	2101	GGTCCGTGAGGTGCCCC TCCGGGAGATGACGGACCAC TGT TGGCCCTCATCTCCCCACG
AL512306	105056	GGTCCGTGAGGTGCCCC TCCGGGAGATGACGGACCAC TGT TGGCCCTCATCTCCCCACG
DNA37151	2161	AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGC TGCATTGCCGGGC
AL512306	104996	AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGC TGCATTGCCGGGC
DNA37151	2221	ACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC
AL512306	104936	ACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC
DNA37151	2281	TGCCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCC TGGAGCTGCGGAGGGT
AL512306	104876	TGCCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCC TGGAGCTGCGGAGGGT
DNA37151	2341	GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGGGCTGACAC
AL512306	104816	GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGGGCTGACAC
DNA37151	2401	TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACA
AL512306	104756	TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACA
DNA37151	2461	GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTAC
AL512306	104696	GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTAC
DNA37151	2521	CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTCCGGGGCCA
AL512306	104636	CCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTCCGGGGCCA
DNA37151	2581	GGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTACAACATTACCCGCCT
AL512306	104576	GGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTACAACATTACCCGCCT
DNA37151	2641	CCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCACACCCA
AL512306	104516	CCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCACACCCA
DNA37151	2701	GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGA
AL512306	104456	GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGA

BLAST RESULTS A-15

DNA37151	2761	TCGTCC TGGGCTCATTGCCATCCTGGCTCTCGCTGTCTTCTCTCTGGCAGCTGGGCTAGC
AL512306	104396	CCGTCC TGGGCTCATTGCCATCCTGGCTCTCGCTGTCTTCTCTCTGGCAGCTGGGCTAGC
DNA37151	2821	GGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCTCTCCCTCC
AL512306	104336	GGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCTCTCCCTCC
DNA37151	2881	AGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGTGTCTGCTCCCCCTCGT
AL512306	104276	AGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGTGTCTGCTCCCCCTCGT
DNA37151	2941	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC
AL512306	104216	CCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC
DNA37151	3001	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
AL512306	104156	ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
DNA37151	3061	CTACTTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
AL512306	104096	CTACTTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
DNA37151	3121	ACCCACGTGCTTGAGGCCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGGCCCTGGGG
AL512306	104036	ACCCACGTGCTTGAGGCCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGGCCCTGGGG
DNA37151	3181	GTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATTC
AL512306	103976	GTGCTTCTGCAGCCTCGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATTC
DNA37151	3241	TGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT
AL512306	103916	TGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT
DNA37151	3301	CTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTG
AL512306	103856	CTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTG
DNA37151	3361	CACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGCCTCCTGGG
AL512306	103796	CACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGCCTCCTGGG
DNA37151	3421	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGTGGGAGTGA
AL512306	103736	CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGTGGGAGTGA
DNA37151	3481	CCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCCAGGAACGCCTCATCTCAGCA
AL512306	103676	CCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCCAGGAACGCCTCATCTCAGCA
DNA37151	3541	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
AL512306	103616	GCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
DNA37151	3601	ATGTGTACCTCCCCCAACCCGATTCACCTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATA
AL512306	103556	ATGTGTACCTCCCCCAACCCGATTCACCTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATA
DNA37151	3661	AATAATAACAATAA
AL512306	103496	AATAATAACAATAA

BLAST RESULTS A-10

>5 NM_006338 Homo sapiens glioma amplified on chromosome 1 protein (3227 bp) [1 seg]

Score = 3002 (5951 bits), Expect = 0.0

Identities = 3017/3022 (99%), at 653,161-3674,3182, Strand +/-

DNA37151	653	AGGGCTGCCCCCTGATGGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGA

NM_006338	161	AGGGCTGCCCCCTGATGGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGA
DNA37151	713	AGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCCGGTGTAGAATGACTGCCCTGGGA

NM_006338	221	AGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCCGGTGTAGAATGACTGCCCTGGGA
DNA37151	773	GGGTGGTTCCCTTGGGCCCTGGCAGGGTTGCTGACCCTTACCCTGCAAAACACAAAGAGCA

NM_006338	281	GGGTGGTTCCCTTGGGCCCTGGCAGGGTTGCTGACCCTTACCCTGCAAAACACAAAGAGCA
DNA37151	833	GGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTC

NM_006338	341	GGACTCCAGACTCTTCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTC
DNA37151	893	GTGGCCCCACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCC

NM_006338	401	GTGGCCCCACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCCGTGTGCCCGTGGTACCC
DNA37151	953	TGGCATGTTCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGC

NM_006338	461	TGGCATGTTCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGC
DNA37151	1013	TCGTCTTACCGCGAGGC'TACCAC'TGTGGACTGCAATGACCTATTCCTGACGGCAGTCCCC

NM_006338	521	TCGTCTTACCGCGAGGC'TACCAC'TGTGGACTGCAATGACCTATTCCTGACGGCAGTCCCC
DNA37151	1073	CCGGCACTCCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTG

NM_006338	581	CCGGCACTCCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTG
DNA37151	1133	GACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGC

NM_006338	641	GACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGC
DNA37151	1193	TTTTCGGATGCCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTA

NM_006338	701	TTTTCGGATGCCCCGAGACTGTGATTTCCATGCCCTTCCCCAGCTGCTGAGCCTGCACCTA
DNA37151	1253	GAGGAGAACCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAG

NM_006338	761	GAGGAGAACCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAG
DNA37151	1313	GAACCTCTATCTCAACCACAACCAGCTCTACCGCATCGCCCCAGGGCCTTTTCTGGCCTC

NM_006338	821	GAACCTCTATCTCAACCACAACCAGCTCTACCGCATCGCCCCAGGGCCTTTTCTGGCCTC
DNA37151	1373	AGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGG

NM_006338	881	AGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGG
DNA37151	1433	TTTGAAATGCTGCCCCAAGTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATC

NM_006338	941	TTTGAAATGCTGCCCCAAGTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATC
DNA37151	1493	CTGGACATGAACCTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAAC

NM_006338	1001	CTGGACATGAACCTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAAC

BLAST RESULTS A-17

DNA37151	1553	CTGCGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC
NM_006338	1061	CTGCGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC
DNA37151	1613	TATGACAACCAGCTGGCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAG
NM_006338	1121	TATGACAACCAGCTGGCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAG
DNA37151	1673	TTCCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATG
NM_006338	1181	TTCCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATG
DNA37151	1733	CTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTT
NM_006338	1241	CTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTT
DNA37151	1793	GCCCTGGTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCC
NM_006338	1301	GCCCTGGTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCC
DNA37151	1853	TTCATCCACCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAAC
NM_006338	1361	TTCATCCACCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAAC
DNA37151	1913	AACGCTCTCAGTGCCCTTGACCAGCAGACGGTGGAGTCCC TGCCCAACCTGCAGGAGGTA
NM_006338	1421	AACGCTCTCAGTGCCCTTGACCAGCAGACGGTGGAGTCCC TGCCCAACCTGCAGGAGGTA
DNA37151	1973	GGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGC
NM_006338	1481	GGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGCCAATGCCACGGGC
DNA37151	2033	ACCCGTGTCCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAG
NM_006338	1541	ACCCGTGTCCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAG
DNA37151	2093	CGCCTCCCGGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCTCATC
NM_006338	1601	CGCCTCCCGGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCTCATC
DNA37151	2153	TCCCCACGAAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCAT
NM_006338	1661	TCCCCACGAAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCAT
DNA37151	2213	TGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGA
NM_006338	1721	TGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGA
DNA37151	2273	CTGACACCTGCCCATGCAGGCAGGAGGTACCGGGTGTAACCCGAGGGGACCCTGGAGCTG
NM_006338	1781	CTGACACCTGCCCATGCAGGCAGGAGGTGCCGGGTGTACCCGAGGGGACCCTGGAGCTG
DNA37151	2333	CGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGG
NM_006338	1841	CGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGG
DNA37151	2393	GCTGACACTAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGAC
NM_006338	1901	GCTGACACTAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGAC
DNA37151	2453	GAAGGACAGGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCT
NM_006338	1961	GAAGGACAGGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCT

BLAST RESULTS A-10

DNA37151	2513	TGGGTCACCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTC
NM_006338	2021	TGGGTCACCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTC
DNA37151	2573	CGGGGCCAGGGGGCCACAGCTCTGGCCCCGCTGCCTCGGGGAACCCACAGCTACAACATT
NM_006338	2081	CGGGGCCAGGGGGCCACAGCTCTGGCCCCGCTGCCTCGGGGAACCCACAGCTACAACATT
DNA37151	2633	ACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCC
NM_006338	2141	ACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCC
DNA37151	2693	CACACCCAGTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCC
NM_006338	2201	CACACCCAGTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCC
DNA37151	2753	TTAGGGGATCGTCTGGGCTCATTGCCATCCTGGCTCTCGCTGTCTTCTCCTGGCAGCT
NM_006338	2261	TTAGGGGATCGTCTGGGCTCATTGCCATCCTGGCTCTCGCTGTCTTCTCCTGGCAGCT
DNA37151	2813	GGGCTAGCGGGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCT
NM_006338	2321	GGGCTAGCGGGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCT
DNA37151	2873	CTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTTGTGTCTGCT
NM_006338	2381	CTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTTGTGTCTGCT
DNA37151	2933	CCCCTCGTCTGCCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACA
NM_006338	2441	CCCCTCGTCTGCCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACA
DNA37151	2993	CTGTTGCCACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAAT
NM_006338	2501	CTGTTGCCACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAAT
DNA37151	3053	CACTAGGACTACTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAG
NM_006338	2561	CACTAGGACTACTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAG
DNA37151	3113	GGACATGGACCCACGTGCTTGAGGCCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGG
NM_006338	2621	GGACATGGACCCACGTGCTTGAGGCCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGG
DNA37151	3173	CCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGC
NM_006338	2681	CCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGC
DNA37151	3233	TGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTC
NM_006338	2741	TGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTC
DNA37151	3293	CCCATCTTCTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCCTACCTGTGTCC
NM_006338	2801	CCCATCTTCTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCCTACCTGTGTCC
DNA37151	3353	CCGGGCTGCACCCCTTCTCTTCTCTTCTCTGTACAGTCTCAGTTGCTTGCTCTTTGTGC
NM_006338	2861	CCGGGCTGCACCCCTTCTCTTCTCTTCTCTGTACAGTCTCAGTTGCTTGCTCTTTGTGC
DNA37151	3413	CTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGT
NM_006338	2921	CTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGT

BLAST RESULTS A-19

DNA37151 3473 GGGAGTGACCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCTCA

 NM_006338 2981 GGGAGTGACCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCTCA
 DNA37151 3533 TCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTT

 NM_006338 3041 TCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTT
 DNA37151 3593 GTGGAGAAATGTGTACCTCCCCCAACCCGATTCACTCTTTTCTCTGTGTTTGTAAAAA

 NM_006338 3101 GTGGAGAAATGTGTACCTCCCCCAACCCGATTCACTCTTTTCTCTGTGTTTGTAAAAA
 DNA37151 3653 TAAAAATAATAATAACAATAA

 NM_006338 3161 TAAAAATAATAATAACAATAA

>6 AF030435 Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA
 (3227 bp) [1 seg]
 Score = 3002 (5951 bits), Expect = 0.0
 Identities = 3017/3022 (99%), at 653,161-3674,3182, Strand +/-

DNA37151 653 AGGGCTGCCCCTGATGGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGA

 AF030435 161 AGGGCTGCCCCTGATGGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGA
 DNA37151 713 AGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCCGGTGTAGAATGACTGCCCTGGGA

 AF030435 221 AGAGAAGGCATATTGAGGAGGGCAAGAAGTGACGCCCGGTGTAGAATGACTGCCCTGGGA
 DNA37151 773 GGGTGGTTCCCTGGGGCCCTGGCAGGGTTGCTGACCCTTACCCTGCAAAACACAAAGAGCA

 AF030435 281 GGGTGGTTCCCTGGGGCCCTGGCAGGGTTGCTGACCCTTACCCTGCAAAACACAAAGAGCA
 DNA37151 833 GGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTC

 AF030435 341 GGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTC
 DNA37151 893 GTGGCCCCACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCCGTGGTACCC

 AF030435 401 GTGGCCCCACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCCGCTGTGCCCCGTGGTACCC
 DNA37151 953 TGGCATGTTCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGC

 AF030435 461 TGGCATGTTCCCTGCCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGC
 DNA37151 1013 TCGTCCTACCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCCCTGACGGCAGTCCCC

 AF030435 521 TCGTCCTACCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCCCTGACGGCAGTCCCC
 DNA37151 1073 CCGGCACTCCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTG

 AF030435 581 CCGGCACTCCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTG
 DNA37151 1133 GACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCAGAACAGC

 AF030435 641 GACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCAGAACAGC
 DNA37151 1193 TTTTCGGATGCCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTA

 AF030435 701 TTTTCGGATGCCCCGAGACTGTGATTTCCATGCCCTTCCCCAGCTGCTGAGCCTGCACCTA
 DNA37151 1253 GAGGAGAACCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAG

BLAST RESULTS A-20

AF030435 761 GAGGAGAACCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAG

DNA37151 1313 GAACTCTATCTCAACCACAACCAGCTCTACCGCATCGCCCCAGGGCCTTTTCTGGCCTC

AF030435 821 GAACTCTATCTCAACCACAACCAGCTCTACCGCATCGCCCCAGGGCCTTTTCTGGCCTC

DNA37151 1373 AGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGG

AF030435 881 AGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGG

DNA37151 1433 TTTGAAATGCTGCCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATC

AF030435 941 TTTGAAATGCTGCCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATC

DNA37151 1493 CTGGACATGAACCTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAAC

AF030435 1001 CTGGACATGAACCTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAAC

DNA37151 1553 CTGCGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC

AF030435 1061 CTGCGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC

DNA37151 1613 TATGACAACCAGCTGGCCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAG

AF030435 1121 TATGACAACCAGCTGGCCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAG

DNA37151 1673 TTCCCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATG

AF030435 1181 TTCCCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATG

DNA37151 1733 CTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTT

AF030435 1241 CTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTT

DNA37151 1793 GCCCTGGTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCC

AF030435 1301 GCCCTGGTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCC

DNA37151 1853 TTCATCCACCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAAC

AF030435 1361 TTCATCCACCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAAC

DNA37151 1913 AACGCTCTCAGTGCCCTTGCAACAGCAGACGGTGGAGTCCC TGCCCAACCTGCAGGAGGTA

AF030435 1421 AACGCTCTCAGTGCCCTTGCAACAGCAGACGGTGGAGTCCC TGCCCAACCTGCAGGAGGTA

DNA37151 1973 GGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGGCAATGCCACGGGC

AF030435 1481 GGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTTCATCCGCTGGGGCAATGCCACGGGC

DNA37151 2033 ACCCGTGTCCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAG

AF030435 1541 ACCCGTGTCCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAG

DNA37151 2093 CGCCTCCCGGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCCTCATC

AF030435 1601 CGCCTCCCGGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCCTCATC

DNA37151 2153 TCCCCACGAAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCAT

AF030435 1661 TCCCCACGAAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCAT

DNA37151 2213 TGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGA

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AF030435 1721 TGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGA

DNA37151 2273 CTGACACCTGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCCGAGGGGACCCCTGGAGCTG

AF030435 1781 CTGACACCTGCCCATGCAGGCAGGAGGTGCCGGGTGTACCCCCGAGGGGACCCCTGGAGCTG

DNA37151 2333 CGGAGGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGG

AF030435 1841 CGGAGGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGG

DNA37151 2393 GCTGACACTAAGACGGT TAGTGTGGT TGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGAC

AF030435 1901 GCTGACACTAAGACGGT TAGTGTGGT TGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGAC

DNA37151 2453 GAAGGACAGGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCT

AF030435 1961 GAAGGACAGGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCT

DNA37151 2513 TGGGTCACCCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTC

AF030435 2021 TGGGTCACCCCACCCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTC

DNA37151 2573 CGGGGCCAGGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTACAACATT

AF030435 2081 CGGGGCCAGGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTACAACATT

DNA37151 2633 ACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCC

AF030435 2141 ACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCC

DNA37151 2693 CACACCCAGTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCC

AF030435 2201 CACACCCAGTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCC

DNA37151 2753 TTAGGGGATCGTCTTGGGCTCATTTGCCATCCTGGCTCTCGCTGTCTTCTCCTGGCAGCT

AF030435 2261 TTAGGGGATCGTCTTGGGCTCATTTGCCATCCTGGCTCTCGCTGTCTTCTCCTGGCAGCT

DNA37151 2813 GGGCTAGCGGGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCT

AF030435 2321 GGGCTAGCGGGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCT

DNA37151 2873 CTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGTGTCTGCT

AF030435 2381 CTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGTGTCTGCT

DNA37151 2933 CCCCTCGTCC TGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACA

AF030435 2441 CCCCTCGTCC TGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACA

DNA37151 2993 CTGTTGCCACCATTTGTCTCAAAATTC TTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAAT

AF030435 2501 CTGTTGCCACCATTTGTCTCAAAATTC TTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAAT

DNA37151 3053 CACTAGGACTACTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAG

AF030435 2561 CACTAGGACTACTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAG

DNA37151 3113 GGACATGGACCCACGTGCTTGAGGCC TGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGG

AF030435 2621 GGACATGGACCCACGTGCTTGAGGCC TGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGG

DNA37151 3173 CCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGC

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AF030435	2681	CCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGC
DNA37151	3233	TGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTC *****
AF030435	2741	TGCCATTCTGAGGAACATCTCCAAGGAACGGGAGGGACTTTGGCTAGAGCCTCCTGCCTC
DNA37151	3293	CCCATCTTCTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCCTACCTGTGTCC *****
AF030435	2801	CCCATCTTCTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCCTACCTGTGTCC
DNA37151	3353	CCGGGCTGCACCCCTTCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGC *****
AF030435	2861	CCGGGCTGCACCCCTTCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGC
DNA37151	3413	CTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGT *****
AF030435	2921	CTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGT
DNA37151	3473	GGGAGTGACCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCTCA *****
AF030435	2981	GGGAGTGACCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCTCA
DNA37151	3533	TCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTT *****
AF030435	3041	TCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTT
DNA37151	3593	GTGGAGAAATGTGTACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAA *****
AF030435	3101	GTGGAGAAATGTGTACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAA
DNA37151	3653	TAAAAATAAATAATAACAATAA *****
AF030435	3161	TAAAAATAAATAATAACAATAA

BLAST RESULTS A-23

RECEIVED

(B)

Tue Jul 17 13:25:00 2001 [BLASTP 2.1.3 [Apr-1-2001]], NABR 0 5 2002
/home/ruby/va/Molbio/carpenda/temp1/pl.DNA37151 (713 aa)

TECH CENTER 1600/2900

Sequences producing High-scoring Segment Pairs:	Score	Match	Pct	E-val
1 P_AAB80253 Human PRO293 protein - Homo sapiens.	3732	713	100	0.0
2 P_AAY13385 protein PRO293 - Homo sapiens.	3732	713	100	0.0
3 NP_006329.1 glioma amplified on chromosome 1 protein (3718	711	100	0.0
4 GAC1_HUMAN Glioma amplified on chromosome 1 protein p	3718	711	100	0.0

>1 P_AAB80253 Human PRO293 protein - Homo sapiens. (713 aa) [1 seg]
Score = 3732 (1442 bits), Expect = 0.0
Identities = 713/713 (100%), Positives = 713/713 (100%), at 1,1-713,713

DNA37151	1	MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL
P_AAB80253	1	MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL
DNA37151	61	TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL
P_AAB80253	61	TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL
DNA37151	121	SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI
P_AAB80253	121	SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI
DNA37151	181	DSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE
P_AAB80253	181	DSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE
DNA37151	241	SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS
P_AAB80253	241	SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS
DNA37151	301	IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNAALSALHQQTVESLPN
P_AAB80253	301	IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNAALSALHQQTVESLPN
DNA37151	361	LQEVGLHGNPIRCDVCIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVFPREMTDHC
P_AAB80253	361	LQEVGLHGNPIRCDVCIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVFPREMTDHC
DNA37151	421	LPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG
P_AAB80253	421	LPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG
DNA37151	481	TLELRRVTAAEEAGLYTCVAQNVLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYH
P_AAB80253	481	TLELRRVTAAEEAGLYTCVAQNVLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYH
DNA37151	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA
P_AAB80253	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA
DNA37151	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVG
P_AAB80253	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVG

BLAST RESULTS B-1


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DNA37151 661 GRRPLPPAWAFWGSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPPLSQNS
*****
P_AAB80253 661 GRRPLPPAWAFWGSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

>2 P_AAY13385 protein PRO293 - Homo sapiens. (713 aa) [1 seg]
Score = 3732 (1442 bits), Expect = 0.0
Identities = 713/713 (100%), Positives = 713/713 (100%), at 1,1-713,713

DNA37151 1 MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVCNDLFL
*****
P_AAY13385 1 MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVCNDLFL

DNA37151 61 TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL
*****
P_AAY13385 61 TAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL

DNA37151 121 SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI
*****
P_AAY13385 121 SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI

DNA37151 181 DSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE
*****
P_AAY13385 181 DSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE

DNA37151 241 SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS
*****
P_AAY13385 241 SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS

DNA37151 301 IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPN
*****
P_AAY13385 301 IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPN

DNA37151 361 LQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVVPFREMTHC
*****
P_AAY13385 361 LQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVVPFREMTHC

DNA37151 421 LPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG
*****
P_AAY13385 421 LPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG

DNA37151 481 TLELRRVTAEAEAGLYTCVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPYH
*****
P_AAY13385 481 TLELRRVTAEAEAGLYTCVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPYH

DNA37151 541 ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA
*****
P_AAY13385 541 ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA

DNA37151 601 FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVG
*****
P_AAY13385 601 FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVG

DNA37151 661 GRRPLPPAWAFWGSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPPLSQNS
*****
P_AAY13385 661 GRRPLPPAWAFWGSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

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BLAST RESULTS B-2

BLAST RESULTS B-3

>3 NP_006329.1 glioma amplified on chromosome 1 protein (leucine-rich) - Homo (713 aa) [1 seg]

Score = 3718 (1436 bits), Expect = 0.0

Identities = 711/713 (99%), Positives = 711/713 (99%), at 1,1-713,713

DNA37151	1	MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL

NP_006329.1	1	MRLLVAPLLLAWVAGATAAVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL
DNA37151	61	TAVPPALPAGTQTLTLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL

NP_006329.1	61	TAVPPALPAGTQTLTLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLL
DNA37151	121	SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI

NP_006329.1	121	SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI
DNA37151	181	DSRWFEMPLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE

NP_006329.1	181	DSRWFEMPLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE
DNA37151	241	SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS

NP_006329.1	241	SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS
DNA37151	301	IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPN

NP_006329.1	301	IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPN
DNA37151	361	LQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC

NP_006329.1	361	LQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC
DNA37151	421	LPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG

NP_006329.1	421	LPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG
DNA37151	481	TLELRRVTAEAEAGLYTCVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYH

NP_006329.1	481	TLELRRVTAEAEAGLYTCVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYH
DNA37151	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA

NP_006329.1	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA
DNA37151	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVG

NP_006329.1	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVG
DNA37151	661	GRRPLPPAWAFWGSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

NP_006329.1	661	GRRPLPPAWAFWGSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

>4 GAC1_HUMAN Glioma amplified on chromosome 1 protein precursor /pid=AAC39792.1 - homo sapiens (713 aa) [1 seg]

Score = 3718 (1436 bits), Expect = 0.0

Identities = 711/713 (99%), Positives = 711/713 (99%), at 1,1-713,713

DNA37151	1	MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL

GAC1_HUMAN	1	MRLLVAPLLLAWVAGATAAVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL
DNA37151	61	TAVPPALPAGTQTHLLQSNISVRVDQSELGYLANLTELDLSQNSFSRDARDCDFHALPQLL

GAC1_HUMAN	61	TAVPPALPAGTQTHLLQSNISVRVDQSELGYLANLTELDLSQNSFSRDARDCDFHALPQLL
DNA37151	121	SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI

GAC1_HUMAN	121	SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI
DNA37151	181	DSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE

GAC1_HUMAN	181	DSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE
DNA37151	241	SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS

GAC1_HUMAN	241	SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS
DNA37151	301	IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETMLNINNALSALHQQTVESLPN

GAC1_HUMAN	301	IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETMLNINNALSALHQQTVESLPN
DNA37151	361	LQEVGLHGNPIRCDVCIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC

GAC1_HUMAN	361	LQEVGLHGNPIRCDVCIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHC
DNA37151	421	LPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG

GAC1_HUMAN	421	LPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG
DNA37151	481	TLELRRVTAEAGLYTCVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPYH

GAC1_HUMAN	481	TLELRRVTAEAGLYTCVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPYH
DNA37151	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA

GAC1_HUMAN	541	ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA
DNA37151	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVG

GAC1_HUMAN	601	FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVG
DNA37151	661	GRRPLPPAWAFWGSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

GAC1_HUMAN	661	GRRPLPPAWAFWGSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

BLAST RESULTS B-A